

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/561,834  
Source: 1FW0  
Date Processed by STIC: 6/7/06

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IFWO

## RAW SEQUENCE LISTING

DATE: 06/07/2006

PATENT APPLICATION: US/10/561,834

TIME: 08:47:51

Input Set : A:\2006-05-22 1254-0301PUS1.txt

Output Set : N:\CRF4\06072006\J561834.raw

3 <110> APPLICANT: Shigeru NAKANO

5 <120> TITLE OF INVENTION: GENE INVOLVED IN GROWTH-PROMOTING FUNCTION OF ACETIC ACID BACTERIA AND

6 USES THEREOF

8 <130> FILE REFERENCE: 1254-0301PUS1

10 <140> CURRENT APPLICATION NUMBER: US 10/561,834

11 <141> CURRENT FILING DATE: 2005-12-22

13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/008797

14 <151> PRIOR FILING DATE: 2004-06-16

16 <150> PRIOR APPLICATION NUMBER: JP 2003-183047

17 <151> PRIOR FILING DATE: 2003-06-26

19 <160> NUMBER OF SEQ ID NOS: 7

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 2352

23 <212> TYPE: DNA

24 <213> ORGANISM: Gluconacetobacter entanii

26 <400> SEQUENCE: 1

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30	tgcgtcttcg	catggtatta	ctggcgactg	cacttggcgc	agcgccattc	gccaccgcaa	240
31	tggccacgac	gattacaggg	ccatatgtcg	atatcggtgg	cgggtatgac	ctgaccaga	300
32	cccagcatgc	ccatggcttt	gacaagaacc	agtacgaaaa	caacgcaa	acggccgggt	360
33	atcttgatgc	aacggacaac	gcccgcctgc	tgaaggaagc	ccattcacgc	gaacgcatgg	420
34	aacatggcga	tggctggacc	ggcttcgcc	cgttcggctg	ggggttcggc	aacggcctgc	480
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37	gcggattcgt	caacgtcctg	tatgacatcg	acctcaagcg	cctgtttaac	attgacgtgc	660
38	ccgtgacacc	attcgctcggc	gttggcgccg	gttacctgtg	gcagaacgtg	gatgccagca	720
39	catccgtgac	ccgctacctg	aacgtgcgcc	agaacggcac	gaatggcagc	ttcgcctatc	780
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41	aataccgcat	gatcggacag	gtggaatcct	tcgccatggg	caatatcagc	cagactggcg	900
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50	gcacataact	gcaataaatt	gataaatagg	cttttttaca	aaggggcgca	caggatgcgc	1440
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56 caagataggg ctctgccctg caacaacaga gttaaggact gaaacatgcg tcttcgcgca 1800
57 gcgttactgg ctaccagcct gctggcagcg gcaccgttcg ccgccaaagc cacgaccatc 1860
58 accggcccgt atgtcgatat cggcggcggc tacaacctga cccagaccca gcacgggcac 1920
59 tttgccgaca cggaagacgg cccggggccgc gaaaagctgg gccaccgtca tggctggacc 1980
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61 tacaactggt ccgaaatcta cagcaagtcc cgtaatgaca agggcagcga ccgctcctat 2100
62 ggcggtttcg tcaacgtgct gtatgacatc gacctgaagc gtctgttcaa catcgacgtg 2160
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64 agcgtgggca acagccccgg tcgcagcctg agcggcacca agggcggctt cgcctaccag 2280
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66 taccgcatga tc                                     2352

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69 <211> LENGTH: 399
70 <212> TYPE: PRT
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82 Gly Gly Gly Tyr Asp Leu Thr Gln Thr Gln His Ala His Gly Phe Asp
83 35 40 45
86 Lys Asn Gln Tyr Glu Asn Asn Ala Asn Thr Ala Gly Tyr Leu Asp Ala
87 50 55 60
90 Thr Asp Asn Ala Arg Leu Leu Lys Glu Ala His Ser Arg Glu Arg Met
91 65 70 75 80
94 Glu His Gly Asp Gly Trp Thr Gly Phe Ala Thr Phe Gly Trp Gly Phe
95 85 90 95
98 Gly Asn Gly Leu Arg Ala Glu Ile Glu Gly Asp Tyr Asn Trp Ser Ala
99 100 105 110
102 Leu Thr Gly Tyr Asn Ser Val Ser Gly Ser Ala Tyr Gly Asn Asn His
103 115 120 125
106 Gln Ser Gly Lys Ser Ser Gly Ser Asp Arg Ser Tyr Gly Gly Phe Val
107 130 135 140
110 Asn Val Leu Tyr Asp Ile Asp Leu Lys Arg Leu Phe Asn Ile Asp Val
111 145 150 155 160
114 Pro Val Thr Pro Phe Val Gly Val Gly Ala Gly Tyr Leu Trp Gln Asn
115 165 170 175
118 Val Asp Ala Ser Thr Ser Val Thr Arg Tyr Leu Asn Val Arg Gln Asn
119 180 185 190
122 Gly Thr Asn Gly Ser Phe Ala Tyr Gln Gly Met Val Gly Ala Ala Tyr
123 195 200 205
126 Asp Ile Pro Gly Val Pro Gly Leu Gln Met Thr Thr Glu Tyr Arg Met
127 210 215 220
130 Ile Gly Gln Val Glu Ser Phe Ala Met Gly Asn Ile Ser Gln Thr Gly
131 225 230 235 240
134 Gly Gly Asp Arg Thr Leu Ser Tyr Asp His Arg Phe Asn His Gln Phe

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139           260           265           270
142 Pro Ala Pro Ala Val Ala Pro Pro Ala Pro Ser Ala Ala Arg Thr Tyr
143           275           280           285
146 Leu Val Phe Phe Asp Trp Asp Gly Ala Val Leu Thr Asp Arg Ala Arg
147           290           295           300
150 Gly Ile Val Ala Glu Ala Ala Gln Ala Ser Thr His Val Gln Thr Thr
151 305           310           315           320
154 Arg Ile Glu Val Asn Gly Tyr Thr Asp Asn Thr Ser Ala His Pro Gly
155           325           330           335
158 Pro Arg Gly Glu Lys Tyr Asn Leu Gly Leu Ser Met Arg Arg Ala Asp
159           340           345           350
162 Ser Val Lys Ala Glu Leu Ile Arg Asp Gly Val Pro Ala Gly Gly Ile
163           355           360           365
166 Asp Ile His Trp Tyr Gly Glu Ala His Pro Leu Val Val Thr Gln Pro
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184 <400> SEQUENCE: 3
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189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial sequence: synthetic
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196 <400> SEQUENCE: 4
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200 <211> LENGTH: 5734
201 <212> TYPE: DNA
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207 gcaccttctg ctaccccacc cagaacgcca gcggttgggc tgtgcagcca tgatcgccaa           180
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214	gggatgcggt	cggacggctc	tacgtccaga	tcaagaacct	caccacccca	gaccccgga	600
215	ccacggagcc	gttcgtcatg	atccgtcccg	cccagaatcg	cgccgtcacc	ctctggctgc	660
216	tgaagaacag	taagcggccc	atgaaggccg	tggacgtatg	gacgctgctg	ttcgaccacc	720
217	tgtttcccca	taccggccag	atcatgctga	cccgtgagga	aatcgcgga	aaagtcggta	780
218	tccgggtcaa	cgaagttaca	gccgtcatga	acgagctggt	gagcttcggc	gcgattttct	840
219	ccgagcgcga	gaaggtggcc	ggaatgcgcg	ggccgggccc	cgcccgcctc	tacatgaacc	900
220	ggcatgtggc	cgaggtcggc	agccgcgcga	cgcaggaaga	acttgcccta	atcccacgcc	960
221	ccggcgccaa	gctggcagtc	gtgcagggtg	gcaaggctta	acccatgaag	gtttcggaac	1020
222	tggacgtgtt	cgacagcgcc	aaggcggcac	aagaccggtt	ggtgcgggaa	gaactgctgc	1080
223	aagcagcgca	ggcggacggc	cacggccccg	ccctcgctca	tgcccgttcc	gtcatagcca	1140
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258	tctgtaagcg	gatgcgggga	cgagacaagc	ccgtcagggc	gcgtcagcgg	gtgttgccgg	3240
259	gtgtcggggc	tggcttaact	atgcggcatc	agagcagatt	gtactgagag	tgcaccatat	3300
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